

SEQUENCE LISTING

<110> Levinson, Douglas A.
Lloyd, Clare M.
McCarthy, Sean A.

<120> COMPOSITIONS AND METHODS FOR THE TREATMENT AND
DIAGNOSIS OF IMMUNE DISORDERS

<130> 7853-125

<140> 09/324,986

<141> 1999-06-02

<150> 09/032,337

<151> 1998-02-27

<150> 08/609,583

<151> 1996-03-01

<150> 08/487,748

<151> 1995-06-07

<150> 08/398,633

<151> 1995-03-05

<160> 49

<170> PatentIn Ver. 2.0

<210> 1

<211> 357

<212> DNA

<213> Mus musculus

<400> 1

```
ctgggtgagg ggatctacaa cttgttcggt taaagaaaaa agcaacagcc aacagaaatg 60
tggttatect tcacctacct aaaaaggagg atgatgtgaa accaggaacc agatgccgag 120
tagcaggatg ggggagattt ggcaataagt cagctccctc tgaaactctg agagaagtca 180
acatcactgt catagacaga aaaatctgca atgatgaaaa acatataat ttctatctctg 240
taattgtgtc aaacatgatt tgggcagggg acctccccgg cggaaaggac tcctgcaatg 300
gggattcttg cagccctctc ctatgtgatt ggtatttggg aagcatcacc tcctttt 357
```

<210> 2

<211> 255

<212> DNA

<213> Mus musculus

<400> 2

```
ttagcgccat tgccatagag agacctcagc catcaatcac tagcacatga ttgacagaca 60
```

gagaatggga ctttgggctt tggcaattct gacacttccc atgtatttga cagttacgga 120
 gggcagtaaa tcgtctctgg gtctggaaaa tgaggcttta attgtgagat gccccaaag 180
 aggacgctcg acttatectg tggaaatggta ttactcagat acaaatgaaa gtattctctac 240
 ccaaaaaaaaa aaaaa 255

<210> 3

<211> 2055

<212> DNA

<213> Mus musculus

<400> 3

cggggtcgac ccaacgctcc gagcctcctc agtcaagaga agcatccctc cagaacacgg 60
 gaaacatgac actttttgaa gaatgccaaa cggcgtgaaa ataaaaacag agcattccca 120
 ttgtcaccga ccaatctcca atctcctgta agattcaaaa gggcagcaaa gaggcgtgta 180
 ccgttcacga aagctaaaat cccatgctat tgaacatgaa gacttctgat gcttaaatct 240
 cattaactgc ttttaagtac tcccaggagc ttggatccca acttctagca gtaatagtct 300
 gtgtaaaaaa aaaaaaaaaa tcagtctaca accactctct aatgcatgg atgaactcat 360
 cagaacatca aaacccaagg aaaccctaag agagaagaat tctaataaaa agaattttac 420
 attgaaaact tacaaggcaa ggtecccttc cctgctgaca gcctaagaag tgatgtaact 480
 gccactgtga agaccatggc gatgaacagc atgtgcattg aagagcagcg ccacctcgaa 540
 cactatttgt tcccggtggt ctacataatt gtgtttatag tcagcgtccc agccaacatc 600
 ggatctttat gcgtatcctt tctgcaagcg aagaaggaaa atgagctagg gatttacctc 660
 ttcagtctgt cctgtcaga cctgctgtat gcgtgactc tgcccctctg gatcaattac 720
 acttgggaata aagacaactg gactttctct ccacacttgt gcaaagggaag cgttttcttc 780
 acctacatga acttttacag cagcacggcg ttctcactt gcattgcctt ggaccgctat 840
 ttagcagtcg tctacctctc gaagttttcc ttcttaagaa cgagaagatt cgcgtttatt 900
 accagcctct ccatctggat attagagtc tcttttaact ctatgctctt gtggaagat 960
 gaaacagatg ttgaatatgt tgactcggac aaatctaatt tcactctctg ctatgacaaa 1020
 taccctctgg agaaatggca gataaacctc aacctgttcc ggacgtgcatt gggctacgca 1080
 atacccttga tcaccatcat gatctgcaac cataaagtct accgagctgt ggcgcacaa 1140
 caagccacgg aaaaacagca gaagagaagg atcataaagt tgcttgctag catcacgttg 1200
 actttcgtcc tatgtcttac ccccttcac gtgatggtgc tcatccgctg cgttttagag 1260
 cgcgacatga acgtcaatga caagtctgga tggcagacgt ttacgggtgta cagagtcaca 1320

gtagccctga cgagtctaaa ctgtgttgcc gatcccatc tgtactgctt tgtgactgag 1380
 accggggagag ctgatatgtg gaacatatta aaattgtgta ctaggaaaca caatagacac 1440
 caagggaaaa aaagggacat actttctgtg tccacaagag atgctgtaga attagagatt 1500
 atagactaag aggtggaggc aggttaagtt acatgggtatt atttaaatgaa acttacattt 1560
 tggaaaagaa atctggcata gtagaaccca gtggaatatg tttgaaggta cattgtatga 1620
 ctccatgtt ggcttttatta agtaaggat agaaatgtat tatctgtat gtattctaata 1680
 gactaggcat cattgtttta gtaccaattc tctttgcctc tatgttataa cccctaagaa 1740
 gcacgcggga ctgttcgtct ttaaatcagt ggccattcta tctgactact atgacttttt 1800
 gttgtgttgc tgccttgggt ttccagtcct cctgcatcag tcttctcctc tgtatacgtc 1860
 tgtcttcaac aaatgtaagg actaaatacc cctccgatc acatccatta tcaaggattt 1920
 gaagccactc catgtactgg gttataaaag aaatgttctc atgaactttc atgaagttaa 1980
 cataccttg gggatctagt cacogagtca cataaagtaa aagtaaatgg aaaaaaaaaa 2040
 aaaaaaaaaa agggc 2055

<210> 4
 <211> 460
 <212> DNA
 <213> Mus musculus

 <220>
 <221> modified_base
 <222> all "n" positions
 <223> n=a, c, g, or t

<400> 4
 cgccagtgtg ctggaattcg gcttagagca tttctttcaa accacaggtt aacacacact 60
 tactaaaaag caatgctgtt agaggagaag ggcttgggag actcggccat ttgaaacana 120
 agcaaggcac tctccaggnn cagcaagtgg attcccattt cctgctgagg gcgggttcac 180
 actgagactg cactccagtc agcgggagga atcacctgca ttaatgcttg tctctcgag 240
 agctagtgtg ccttccactc tgggtacact tgggtgtcaa catttcaaaa tgatgacct 300
 agaggctctc atagtgtgtg ataactatgg naggacagaa gaacactggc tgtattgtct 360
 tttcttttca gcactagtgt cttggccctt aactaaaacg ggttccatca tcttccaaac 420
 caggaagata gattgttaga caggtccttt cccctcaact 460

<210> 5
 <211> 414
 <212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> all "n" positions

<223> n=a, c, g, or t

<400> 5

```
tttttttttt tngggagagg ctgactga aattacagtt tcagtggaat ttagagaagt 60
aataactgca aaaattttatt tacacacaca cacacacaca cagggcattt tacctgtgta 120
agtgacagttt aatcancccc attaccttat gaccttggtt ggcaatgtct ctaaagcttt 180
aaaaattaaa taaaattaaa aagatgggtt tccatctcat aaaatccctt ttgggaatgg 240
aagacttcct ctttggggtn ttttttagag ggaacaggag gtaactgtta attatttata 300
cattctaata aaccatgaat gcaccacata aaatactgta ctcggggagc aaacactgtn 360
tggggggggtt ctctcttacc agaaggaaca gggggccttt caatggctgt gggc 414
```

<210> 6

<211> 240

<212> DNA

<213> Mus musculus

<220>

<221> modified_base

<222> all "n" positions

<223> n=a, c, g, or t

<400> 6

```
tttnngggac aggggtttcnc tgtgtatctc tggctgtcct ggaactnact ctgtagacca 60
gggtggccctc ganctcagaa atctacctgc ctctccctcc anagtgtctg gattaanggt 120
gtatgccacc aatncccgcc cttaatatat tnntaaacaa cttcatttga atganatatt 180
gacactaccc ttggaataag agtncccgga atgangtaca ggnttcangg aatcatttaa 240
```

<210> 7

<211> 217

<212> DNA

<213> Mus musculus

<400> 7

```
cttagcaggt ggagttgcag caggaagcct ggtagccaca ctccaatcag caggggtcct 60
tggactctcc acatcaacaa atgccatcct aggggctgct ggggcactgt tggagccttg 120
ctctgagctt aggagatgac acttctatca gctcaactca aagcctgtac agactaogca 180
ggagatgaag ttccaaaagg caccttcaga accttca 217
```

<210> 8
 <211> 2710
 <212> DNA
 <213> Mus musculus

<220>
 <221> modified_base
 <222> all "n" positions
 <223> n=a, c, g, or t

<400> 8
 ngtcgaccca cgcgtccgga tttccctcc caagtactca tgttttcagg tcttaccctc 60
 aactgtgtcc tgcgtcgtc gcaactacta cttgcaaggt cattggaaga tgggtataag 120
 gttgaggttg gtaaaaaatgc ctatctgccc tgcagttaca ctctacctac atctggggaca 180
 cttgtgccta tgtcgtgggg caagggatcc tgtccttggt cacagtgtac caatgagttg 240
 ctcagaactg atgaagaaaa tgtgacatat cagaaatcca gcagatacca gctaaagggc 300
 gatctcaaca aaggagatgt gtctctgacg ataaagaatg tgactctgga tgaccatggg 360
 acctactgct cgaggatata gttccctggt cttatgaatg ataaaaaatt agaactgaaa 420
 ttagacatca aagcagccaa ggtcactcca gctcagactg cccatgggga ctctactaca 480
 gcttctccaa gaacctaac cacggagaga aatgggttcag agacacagac actgggtgacc 540
 ctccataata acaatggaac aaaaatttcc acatgggctg atgaaattaa ggactctgga 600
 gaaacgatca gaactgctat ccacattgga gtgggagttc ctgctggggt gacctgggca 660
 cttatcattg gtgtcttaat ccttaaatgg tattcctgta agaaaaagaa gttatcgagt 720
 ttgagcctta ttactctggc caacttcctt ccaggagggt tggcaaatgc aggagcagtc 780
 aggattcgct ctgaggaaaa tatctacacc atcgaggaga acgtatatga agtgaggaga 840
 tcaaatgagt actactgcta cgtcaacagc cagcagccat cctgaccgcc tctggactgc 900
 cactttttaa ggctgcgctt ctttctgac ttgggtattt cctttkttgg aaaactatgt 960
 gatatgtcac ttggcaacct cattggaggt tctgaccaca gccactgaga aaagagttcc 1020
 agttttcttg ggataattaa ctcaaaaggg gattcgactg taactcatgc tacattgaaa 1080
 tgctccattt tatccctgag tttcagggat cggatctccc actccagaga cttcaatcat 1140
 gcgtgttgaa gctcactcgt gctttcatac attaggaatg gttagtgtga tgtctttgag 1200
 acatagaggt ttgtggtata tcogcaaagc tcttgaacag gtatgggggaa taaaggggta 1260
 agataggaag gtgcggtctt tgttgatgtt ggaaaaatctt aaagaagttg gttagctttc 1320
 tagagatttc tgaccttgaa agattaagaa aaagccaggt gccatatgct taacacgata 1380
 taactgggga accttaggca ggagggtgat aagttcaagg tcagccaggg ctatgctggt 1440

aagactgtct camcatccaa agacgaaaat aaacatagag acagcaggag gctggagatg 1500
 aggctcggac agtgagggtgc atttgtgtaca agcacgagga atctatatatt gatcgtagac 1560
 cccacatgaa aaagctaggc ctggttagagc atgcttgtag actcaagaga tggagaggta 1620
 aaggcacaac agatccccgg ggcttgctgtg cagtcagctt agcctagggtg ctgagttcca 1680
 agtcacaag agtcctctgc tcamagtaag atgggrctgag tatctggcgc atgtccatgg 1740
 ggggtgtcct ctctctctcag aagagacatg cacatgwccc tgcacacaca cacacacaca 1800
 cacacacaca cacacacaca cacacacaca tgawatgaag gttctctctg tgcctgctac 1860
 ctctctataa catgtatctc tacaggactc tcctctgcct ctgttaagac atgagtggga 1920
 gcatggcaga gcagtcctag aatttattcc agcactcaga aggctggagc agaagcgtgg 1980
 agagttcagg agcactgtgc ccaacactgc cagactcttc ttacacaaga aaaagggttac 2040
 ccgcaagcag cctgctgtct gtaaaaggaa accctgcgaa aggcacaaact tgactgttgt 2100
 gtgctcaagg ggaactgact cagacaactt ctccattcct ggaggaaact ggagctgttt 2160
 ctgacagaag aacaaccggt gactgggaca tacgaaggca gagctcttgc agcaatctat 2220
 atagtcagca aaatattctt tgggaggaca gtgcgcacca aattgatttc caagccgggtg 2280
 gacctcagtt tcattctggt tacagctgcc tgcccagtcg ccttgatctg tgctggctcc 2340
 catctataac agaatcaaat taaatagacc ccgagtgaat atattaagt agcagaaagg 2400
 tagctttgtt caaagatttt ttgcatgtg ggagcaactg tgtacatcag aggacatctg 2460
 ttagttagga caccaaaacc tgtggtaccg ttttttcatg tatgaatttt gttgtttagg 2520
 ttgctcttag ctagctgtgg aggtcctggc tttcttaggt gggataggaa gggagaccat 2580
 ctaacaaaaa ccattagaga taacagctct catgcagaag ggaaaactaa tctcaaatgt 2640
 tttaaagtaa taaaactgta ctggcaaagt actttgagca taaaaaaaaa aaaaaaaaaa 2700
 gggcgccgc 2710

<210> 9
 <211> 337
 <212> PRT
 <213> Mus musculus

<400> 9
 Met Ala Met Asn Ser Met Cys Ile Glu Glu Gln Arg His Leu Glu His
 1 5 10 15
 Tyr Leu Phe Pro Val Val Tyr Ile Ile Val Phe Ile Val Ser Val Pro
 20 25 30

Ala Asn Ile Gly Ser Leu Cys Val Ser Phe Leu Gln Ala Lys Lys Glu
35 40 45

Asn Glu Leu Gly Ile Tyr Leu Phe Ser Leu Ser Leu Ser Asp Leu Leu
50 55 60

Tyr Ala Leu Thr Leu Pro Leu Trp Ile Asn Tyr Thr Trp Asn Lys Asp
65 70 75 80

Asn Trp Thr Phe Ser Pro Thr Leu Cys Lys Gly Ser Val Phe Phe Thr
85 90 95

Tyr Met Asn Phe Tyr Ser Ser Thr Ala Phe Leu Thr Cys Ile Ala Leu
100 105 110

Asp Arg Tyr Leu Ala Val Val Tyr Pro Leu Lys Phe Ser Phe Leu Arg
115 120 125

Thr Arg Arg Phe Ala Phe Ile Thr Ser Leu Ser Ile Trp Ile Leu Glu
130 135 140

Ser Phe Phe Asn Ser Met Leu Leu Trp Lys Asp Glu Thr Ser Val Glu
145 150 155 160

Tyr Cys Asp Ser Asp Lys Ser Asn Phe Thr Leu Cys Tyr Asp Lys Tyr
165 170 175

Pro Leu Glu Lys Trp Gln Ile Asn Leu Asn Leu Phe Arg Thr Cys Met
180 185 190

Gly Tyr Ala Ile Pro Leu Ile Thr Ile Met Ile Cys Asn His Lys Val
195 200 205

Tyr Arg Ala Val Arg His Asn Gln Ala Thr Glu Asn Ser Glu Lys Arg
210 215 220

Arg Ile Ile Lys Leu Leu Ala Ser Ile Thr Leu Thr Phe Val Leu Cys
225 230 235 240

Phe Thr Pro Phe His Val Met Val Leu Ile Arg Cys Val Leu Glu Arg
245 250 255

Asp Met Asn Val Asn Asp Lys Ser Gly Trp Gln Thr Phe Thr Val Tyr
260 265 270

Arg Val Thr Val Ala Leu Thr Ser Leu Asn Cys Val Ala Asp Pro Ile
275 280 285

Leu Tyr Cys Phe Val Thr Glu Thr Gly Arg Ala Asp Met Trp Asn Ile
290 295 300

Leu Lys Leu Cys Thr Arg Lys His Asn Arg His Gln Gly Lys Lys Arg
305 310 315 320

Asp Ile Leu Ser Val Ser Thr Arg Asp Ala Val Glu Leu Glu Ile Ile
325 330 335

Asp

<210> 10
 <211> 281
 <212> PRT
 <213> Mus musculus

<400> 10
 Met Phe Ser Gly Leu Thr Leu Asn Cys Val Leu Leu Leu Leu Gln Leu
 1 5 10 15
 Leu Leu Ala Arg Ser Leu Glu Asp Gly Tyr Lys Val Glu Val Gly Lys
 20 25 30
 Asn Ala Tyr Leu Pro Cys Ser Tyr Thr Leu Pro Thr Ser Gly Thr Leu
 35 40 45
 Val Pro Met Cys Trp Gly Lys Gly Phe Cys Pro Trp Ser Gln Cys Thr
 50 55 60
 Asn Glu Leu Leu Arg Thr Asp Glu Arg Asn Val Thr Tyr Gln Lys Ser
 65 70 75 80
 Ser Arg Tyr Gln Leu Lys Gly Asp Leu Asn Lys Gly Asp Val Ser Leu
 85 90 95
 Ile Ile Lys Asn Val Thr Leu Asp Asp His Gly Thr Tyr Cys Cys Arg
 100 105 110
 Ile Gln Phe Pro Gly Leu Met Asn Asp Lys Lys Leu Glu Leu Lys Leu
 115 120 125
 Asp Ile Lys Ala Ala Lys Val Thr Pro Ala Gln Thr Ala His Gly Asp
 130 135 140
 Ser Thr Thr Ala Ser Pro Arg Thr Leu Thr Thr Glu Arg Asn Gly Ser
 145 150 155 160
 Glu Thr Gln Thr Leu Val Thr Leu His Asn Asn Asn Gly Thr Lys Ile
 165 170 175
 Ser Thr Trp Ala Asp Glu Ile Lys Asp Ser Gly Glu Thr Ile Arg Thr
 180 185 190
 Ala Ile His Ile Gly Val Gly Val Ser Ala Gly Leu Thr Leu Ala Leu
 195 200 205
 Ile Ile Gly Val Leu Ile Leu Lys Trp Tyr Ser Cys Lys Lys Lys Lys
 210 215 220
 Leu Ser Ser Leu Ser Leu Ile Thr Leu Ala Asn Leu Pro Pro Gly Gly
 225 230 235 240
 Leu Ala Asn Ala Gly Ala Val Arg Ile Arg Ser Glu Glu Asn Ile Tyr
 245 250 255

Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Asn Ser Asn Glu Tyr Tyr
260 265 270

Cys Tyr Val Asn Ser Gln Gln Pro Ser
275 280

<210> 11
<211> 1257
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (22) .. (1137)

<400> 11
ccgggtcgac ccacgcgtcc g atg aca ctg act gcc cac ctc tcc tac ttt 51
Met Thr Leu Thr Ala His Leu Ser Tyr Phe
1 5 10

ctg gtc ctg ttg tta gcg ggc caa ggc ctc agt gac tcc ctc ctc acc 99
Leu Val Leu Leu Leu Ala Gly Gln Gly Leu Ser Asp Ser Leu Leu Thr
15 20 25

aag gat gca ggt ccc cgc cca ctg gag ctg aag gaa gtc ttc aag ctg 147
Lys Asp Ala Gly Pro Arg Pro Leu Glu Leu Lys Glu Val Phe Lys Leu
30 35 40

ttc cag atc cgg ttc aac cgg agt tac tgg aac cca gca gag tac act 195
Phe Gln Ile Arg Phe Asn Arg Ser Tyr Trp Asn Pro Ala Glu Tyr Thr
45 50 55

cgc cgt ctg agc atc ttt gcc cac aat ctg gct cag gct caa agg cta 243
Arg Arg Leu Ser Ile Phe Ala His Asn Leu Ala Gln Ala Gln Arg Leu
60 65 70

cag caa gaa gac ttg ggt aca gct gag ttt gga gag act cca ttc agt 291
Gln Gln Glu Asp Leu Gly Thr Ala Glu Phe Gly Glu Thr Pro Phe Ser
75 80 85 90

gac ctc aca gag gag gag ttt ggc cag tta tac ggg cag gag agg tca 339
Asp Leu Thr Glu Glu Phe Gly Gln Leu Tyr Gly Gln Glu Arg Ser
95 100 105

cca gaa agg acc ccc aac atg acc aaa aag gta gag tct aac acg tgg 387
Pro Glu Arg Thr Pro Asn Met Thr Lys Lys Val Glu Ser Asn Thr Trp
110 115 120

ggg gaa tct gtg ccc cgc acc tgt gac tgg cgt aaa gca aag aac atc 435
Gly Glu Ser Val Pro Arg Thr Cys Asp Trp Arg Lys Ala Lys Asn Ile
125 130 135

atc tcg tcg gtc aag aac cag gga agc tgc aaa tgc tgc tgg gcc atg 483
Ile Ser Ser Val Lys Asn Gln Gly Ser Cys Lys Cys Cys Trp Ala Met
140 145 150

gca gct gcc gac aac atc cag gct ctg tgg cgc atc aaa cac cag cag	531
Ala Ala Ala Asp Asn Ile Gln Ala Leu Trp Arg Ile Lys His Gln Gln	
155 160 165 170	
ttt gtg gac gtc tct gtg cag gag ctg ctg gac tgc gaa cgc tgt gga	579
Phe Val Asp Val Ser Val Gln Glu Leu Leu Asp Cys Glu Arg Cys Gly	
175 180 185	
aat ggt tgc aat ggt ggc ttc gtg tgg gac gca tat cta act gtc etc	627
Asn Gly Cys Asn Gly Gly Phe Val Trp Asp Ala Tyr Leu Thr Val Leu	
190 195 200	
aac aac agt ggc ctg gcc agt gaa aag gat tat cca ttc cag ggg gac	675
Asn Asn Ser Gly Leu Ala Ser Glu Lys Asp Tyr Pro Phe Gln Gly Asp	
205 210 215	
aga aag cct cac aga tgc cta gcc aag aag tac aag aag gtg gcc tgg	723
Arg Lys Pro His Arg Cys Leu Ala Lys Lys Tyr Lys Lys Val Ala Trp	
220 225 230	
atc cag gat ttc acc atg ttg tcc aat aat gag cag gca att gcc cac	771
Ile Gln Asp Phe Thr Met Leu Ser Asn Asn Glu Gln Ala Ile Ala His	
235 240 245 250	
tac ctg gcc gtg cat gga cct atc acc gtg acc atc aac atg aaa cta	819
Tyr Leu Ala Val His Gly Pro Ile Thr Val Thr Ile Asn Met Lys Leu	
255 260 265	
ctc cag cat tac cag aag ggt gtc atc aag gct aca ccc agc tcc tgt	867
Leu Gln His Tyr Gln Lys Gly Val Ile Lys Ala Thr Pro Ser Ser Cys	
270 275 280	
gac cct cgg caa gtg gac cac tct gtc ttg ctg gtg ggc ttt ggc aag	915
Asp Pro Arg Gln Val Asp His Ser Val Leu Leu Val Gly Phe Gly Lys	
285 290 295	
gag aaa gag ggc atg cag aca ggg aca gtc ttg tcc cat tct cga aaa	963
Glu Lys Glu Gly Met Gln Thr Gly Thr Val Leu Ser His Ser Arg Lys	
300 305 310	
cgt cgc cac tcc tcc cca tac tgg atc ctg aag aac tcc tgg gga gct	1011
Arg Arg His Ser Ser Pro Tyr Trp Ile Leu Lys Asn Ser Trp Gly Ala	
315 320 325 330	
cac tgg ggc gag aag ggt tac ttc agg ctg tat cgg gga aac aac acc	1059
His Trp Gly Glu Lys Gly Tyr Phe Arg Leu Tyr Arg Gly Asn Asn Thr	
335 340 345	
tgt gga gtc acc aag tat ccc ttc aca gct caa gtg gac tca cca gta	1107
Cys Gly Val Thr Lys Tyr Pro Phe Thr Ala Gln Val Asp Ser Pro Val	
350 355 360	
aag aag gca cgg acc tct tgt cct ccc tga aggcagcagv cactcttctg	1157
Lys Lys Ala Arg Thr Ser Cys Pro Pro	
265 370	

cttctccac atggccactg ccccttgta gccctgccca catcctctct gtaggcttc 1217
ataaaccaag actgctccgt gaaaaaaaa aaaaaaaaaa 1257

<210> 12
<211> 371
<212> PRT
<213> Mus musculus

<400> 12
Met Thr Leu Thr Ala His Leu Ser Tyr Phe Leu Val Leu Leu Ala
1 5 10 15
Gly Gln Gly Leu Ser Asp Ser Leu Leu Thr Lys Asp Ala Gly Pro Arg
20 25 30
Pro Leu Glu Leu Lys Glu Val Phe Lys Leu Phe Gln Ile Arg Phe Asn
35 40 45
Arg Ser Tyr Trp Asn Pro Ala Glu Tyr Thr Arg Arg Leu Ser Ile Phe
50 55 60
Ala His Asn Leu Ala Gln Ala Gln Arg Leu Gln Gln Glu Asp Leu Gly
65 70 75 80
Thr Ala Glu Phe Gly Glu Thr Pro Phe Ser Asp Leu Thr Glu Glu Glu
85 90 95
Phe Gly Gln Leu Tyr Gly Gln Glu Arg Ser Pro Glu Arg Thr Pro Asn
100 105 110
Met Thr Lys Lys Val Glu Ser Asn Thr Trp Gly Glu Ser Val Pro Arg
115 120 125
Thr Cys Asp Trp Arg Lys Ala Lys Asn Ile Ile Ser Ser Val Lys Asn
130 135 140
Gln Gly Ser Cys Lys Cys Cys Trp Ala Met Ala Ala Asp Asn Ile
145 150 155 160
Gln Ala Leu Trp Arg Ile Lys His Gln Gln Phe Val Asp Val Ser Val
165 170 175
Gln Glu Leu Leu Asp Cys Glu Arg Cys Gly Asn Gly Cys Asn Gly Gly
180 185 190
Phe Val Trp Asp Ala Tyr Leu Thr Val Leu Asn Asn Ser Gly Leu Ala
195 200 205
Ser Glu Lys Asp Tyr Pro Phe Gln Gly Asp Arg Lys Pro His Arg Cys
210 215 220
Leu Ala Lys Lys Tyr Lys Lys Val Ala Trp Ile Gln Asp Phe Thr Met
225 230 235 240
Leu Ser Asn Asn Glu Gln Ala Ile Ala His Tyr Leu Ala Val His Gly
245 250 255

Pro Ile Thr Val Thr Ile Asn Met Lys Leu Leu Gln His Tyr Gln Lys
260 265 270

Gly Val Ile Lys Ala Thr Pro Ser Ser Cys Asp Pro Arg Gln Val Asp
275 280 285

His Ser Val Leu Leu Val Gly Phe Gly Lys Glu Lys Glu Gly Met Gln
290 295 300

Thr Gly Thr Val Leu Ser His Ser Arg Lys Arg Arg His Ser Ser Pro
305 310 315 320

Tyr Trp Ile Leu Lys Asn Ser Trp Gly Ala His Trp Gly Glu Lys Gly
325 330 335

Tyr Phe Arg Leu Tyr Arg Gly Asn Asn Thr Cys Gly Val Thr Lys Tyr
340 345 350

Pro Phe Thr Ala Gln Val Asp Ser Pro Val Lys Lys Ala Arg Thr Ser
355 360 365

Cys Pro Pro
370

<210> 13
<211> 130
<212> PRT
<213> Mus musculus

<400> 13
Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
1 5 10 15

Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
20 25 30

Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
35 40 45

Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
50 55 60

Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
65 70 75 80

Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu
85 90 95

Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Ile Thr Gly Asn Ile Gly
100 105 110

Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
115 120 125

Glu Glu
130

<210> 14
 <211> 130
 <212> PRT
 <213> Mus musculus

<400> 14
 Met Arg Gln Lys Ala Val Ser Val Phe Leu Cys Tyr Leu Leu Leu Phe
 1 5 10 15
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 20 25 30
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 35 40 45
 Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 50 55 60
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 65 70 75 80
 Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Leu Val Ala Thr Leu
 85 90 95
 Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly
 100 105 110
 Ala Leu Met Arg Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp
 115 120 125
 Glu Glu
 130

<210> 15
 <211> 110
 <212> PRT
 <213> Mus musculus

<400> 15
 Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
 1 5 10 15
 Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Leu Ala
 20 25 30
 Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
 35 40 45
 Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
 50 55 60
 Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
 65 70 75 80
 Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
 85 90 95

Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
 100 105 110

<210> 16
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 16
 Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly Phe Trp
 1 5 10 15
 Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val Ala Gly
 20 25 30
 Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn Ser Val
 35 40 45
 Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly Gly Val
 50 55 60
 Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly
 65 70 75 80
 Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr
 85 90 95
 His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
 100 105

<210> 17
 <211> 122
 <212> PRT
 <213> Mus musculus

<400> 17
 Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
 1 5 10 15
 Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
 20 25 30
 Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Met Ala Ala Val Pro
 35 40 45
 Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser
 50 55 60
 Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly
 65 70 75 80
 Gly Val Ala Ser Gly Ser Leu Val Gly Thr Leu Gln Ser Leu Gly Ala
 85 90 95
 Thr Gly Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser
 100 105 110

Ala Ile Ala Ala Val Ile Ala Arg Phe Tyr
115 120

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
ttgccataga gagacctc 18

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
tgctgtccaa ttatacagg 19

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
gaacacggca ttgtcactaa ct 22

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
cctcatagat gggcactgtg t 21

<210> 22
<211> 843
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 22

atgttttcag gtcttacct caactgtgtc ctgctgtgtc tgcaactact acttgcaagg 60
 tcattggaag atggttataa ggttgaggtt ggtaaaaatg cctatctgcc ctgcagttac 120
 actctaccta catctgggac acttgtgcct atgtgtgtgg gcaagggatt ctgtcccttg 180
 tcacagtgt ccaatgagtt gctcagaact gatgaaagaa atgtgacata tcagaaatcc 240
 agcagatacc agctaaagg cgatctcaac aaaggagatg tgtctctgat cataaagaat 300
 gtgactctgg atgacctgg gacctactgc tgcaggatac agttcccttg tcttatgaat 360
 gataaaaaat tagaactgaa attagacatc aaagcagcca aggtcactcc agctcagact 420
 gcccatgggg actctactac agcttctcca agaaccctaa ccacggagag aaatggttca 480
 gagacacaga cactggtgac cctccataat aacaatggaa caaaaattc cacatgggct 540
 gatgaaatta aggactctgg agaaacgac agaactgcta tccacattgg agtgggagtc 600
 tctgtctggg tgaccttggc acttatcatt ggtgtcttaa tcttaaatg gtattcctgt 660
 aagaaaaaga agttatcgag tttagcctt attacactgg ccaactgcc tccaggaggg 720
 ttggcaaatg caggagcagt caggattcgc tctgaggaaa atatctacac catcgaggag 780
 aacgtatatg aagtgaggaa ttcaaatgag tactactgct acgtcaacag ccagcagcca 840
 tcc 843

<210> 23

<211> 2236

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(944)

<400> 23

cgctaacaga ggtgtctctt gactttttct ctgcaagctc c atg ttt tca cat ctt 56
 Met Phe Ser His Leu
 1 5
 ccc ttt gac tgt gtc ctg ctg ctg ctg ctg cta cta ctt aca agg tcc 104
 Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu Leu Thr Arg Ser
 10 15 20
 tca gaa gtg gaa tac aga gcg gag gtc ggt cag aat gcc tat ctg ccc 152
 Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
 25 30 35

tgc ttc tac acc cca gcc gcc cca ggg aac ctc gtg ccc gtc tgc tgg	200
Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp	
40 45 50	
ggc aaa gga gcc tgt cct gtg ttt gaa tgt ggc aac gtg gtg ctc agg	248
Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg	
55 60 65	
act gat gaa agg gat gtg aat tat tgg aca tcc aga tac tgg cta aat	296
Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn	
70 75 80 85	
ggg gat ttc cgc aaa gga gat gtg tcc ctg acc ata gag aat gtg act	344
Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr Ile Glu Asn Val Thr	
90 95 100	
cta gca gac agt ggg atc tac tgc tgc cgg atc caa atc cca ggc ata	392
Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile	
105 110 115	
atg aat gat gaa aaa ttt aac ctg aag ttg gtc atc aaa cca gcc aag	440
Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala Lys	
120 125 130	
gtc acc cct gca ccg act ctg cag aga gac ttc act gca gcc ttt cca	488
Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe Thr Ala Ala Phe Pro	
135 140 145	
agg atg ctt acc acc agg gga cat ggc cca gca gag aca cag aca ctg	536
Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala Glu Thr Gln Thr Leu	
150 155 160 165	
ggg agc ctc cct gat ata aat cta aca caa ata tcc aca ttg gcc aat	584
Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile Ser Thr Leu Ala Asn	
170 175 180	
gag tta cgg gac tct aga ttg gcc aat gac tta cgg gac tct gga gca	632
Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu Arg Asp Ser Gly Ala	
185 190 195	
acc atc aga ata ggc atc tac atc gga gca ggg atc tgt gct ggg ctg	680
Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly Ile Cys Ala Gly Leu	
200 205 210	
gct ctg gct ctt atc ttc ggc gct tta att ttc aaa tgg tat tct cat	728
Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe Lys Trp Tyr Ser His	
215 220 225	
agc aaa gag aag ata cag aat tta agc ctc atc tct ttg gcc aac ctc	776
Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile Ser Leu Ala Asn Leu	
230 235 240 245	
cct ccc tca gga ttg gca aat gca gta gca gag gga att cgc tca gaa	824
Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu Gly Ile Arg Ser Glu	
250 255 260	

gaa aac atc tat acc att gaa gag aac gta tat gaa gtg gag gag ccc 872
 Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr Glu Val Glu Glu Pro
 265 270 275
 aat gag tat tat tgc tat gtc agc agc agg cag caa ccc tca caa cct 920
 Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln Gln Pro Ser Gln Pro
 280 285 290
 ttg ggt tgt cgc ttt gca atg cca tagatccaac caccttattt ttgagcttgg 974
 Leu Gly Cys Arg Phe Ala Met Pro
 295 300
 tgttttgtct ttttcagaaa ctatgagctg tgtcacctga ctgggttttg aggttctgtc 1034
 cactgctatg gaggagagtt tccccatttt cagaagataa tgactcacat gggaattgaa 1094
 ctgggacctg cactgaactt aaacaggcat gtcattgcct ctgtatttaa gccaacagag 1154
 ttaccaaac cagagactgt taatcatgga tgttagagct caaacgggct tttatataca 1214
 ctaggaaatc ttgacgtggg gtctctggag ctccaggaaa ttcgggcaca tcatatgtcc 1274
 atgaaaactc agataaacta gggraaaactg ggtgctgagg tgaaagcata acttttttgg 1334
 cacagaaagt ctaaaggggc cactgatttt caaagagatc tgtgatccct ttttgttttt 1394
 tgtttttgag atggagtctt gctctgttgc ccaggctgga gtgcaatggc acaatctcgg 1454
 ctactgcaa gctccgcctc ctggggtcaa gcgatttctc tgcctcagcc tctgagtg 1514
 ctgggattac aggcattgac caccatgccc agctaatttg ttgtattttt agtagagaca 1574
 ggggtttcacc atgttggtgca gtgtggtctc aaactcctga cctcatgatt tgctgcctc 1634
 ggcctcccaa agcactggga ttacaggcgt gagccaccac atccagccag tgatccttaa 1694
 aagattaaga gatgactgga ctagggtctac ctgtatcttg aagattccct tggaaatgtt 1754
 agatttaggc ttatttgagc actacctgcc caactgtcag tgccagtgca tagcccttct 1814
 tttgtctccc ttatgaagac tgccctgcag ggctgagatg tggcaggagc tcccagggaa 1874
 aaaggaagtg catttgattg gtgtgtattg gccaaagttt gcttgttgtg tgcttgaag 1934
 aaaatatctc tgaccaactt ctgtattcgt ggaccaaact gaagctatat ttttcacaga 1994
 agaagaagca gtgacgggga cacaaaattct gttgcctggg ggaaagaagg caaaggcctt 2054
 cagcaatcta tattaccagc gctggatcct ttgacagaga gtgggtcccta aacttaaatt 2114
 tcaagacggt ataggcttga tctgtcttgc ttattgttgc cccctgcgcc tagcacaatt 2174
 ctgacacaca attggaactt actaaaaaatt tttttttact gttaaaaaaa aaaaaaaaaa 2234
 aa 2236

<210> 24

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 24

```

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
  1              5              10              15

Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
  20              25              30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
  35              40              45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
  50              55              60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
  65              70              75              80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
  85              90              95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
  100             105             110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
  115             120             125

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Leu Gln Arg Asp Phe
  130             135             140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
  145             150             155             160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
  165             170             175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
  180             185             190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
  195             200             205

Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
  210             215             220

Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
  225             230             235             240

Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Gly
  245             250             255

Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Thr Ile Glu Glu Asn Val Tyr
  260             265             270

Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
  275             280             285

```

Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
 290 295 300

<210> 25
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 25
 aaattttattc tcgaggaccc acgcgtccgg atttccc 37

<210> 26
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide oligonucleotide

<400> 26
 ttaatttgga tccccagttc tgatcggttc tcagagtc 39

<210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 27
 aaattttattc tcgagcgcta acagaggtgt cc 32

<210> 28
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 28
 ttaatttgga tcccctctga tggttgctcc agagtccg 39

<210> 29
 <211> 31

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 29
 ccgcgggtac cagtaaatcg tcctgggggtg g 31

 <210> 30
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 30
 aaataaagga tccctacatc cagcaactat gtagta 36

 <210> 31
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 31
 gcgcaattga ctagtgaccc acgcgtccgg atttc 35

 <210> 32
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

 <400> 32
 gacgcggatc ctcaggatgg ctgctggctg 30

 <210> 33
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 33
 gaacacacta gtactatcct gtgccattgc catagaga 38

<210> 34
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 34
 ggaatattgg gcccttggat cccaagtctg cacacctgca ctcc 44

<210> 35
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 35
 gtaaatcgtc ctggggctctg g 21

<210> 36
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 36
 ccttctgata acacaagcat aaatc 25

<210> 37
 <211> 903
 <212> DNA
 <213> Homo sapiens

<400> 37
 atgttttcac atcttccett tgactgtgtc ctgtgtgtgc tgctgtact acttacaagg 60
 tcttcagaag tggaatacag agcggaggtc ggtcagaatg cctatctgcc ctgtcttctac 120
 accccagccg ccccgaggaa cctcgtgccc gtctgtctgg gcaaaggagg. ctgtcctgtg 180
 ttgaaatgtg gcaacgtggt gctcaggact gatgaaaggg atgtgaatta ttggacatcc 240
 agatactggc taaatgggga ttccgcaaa ggagatgtgt cctgaccat agagaatgtg 300

actctagcag acagtgggat ctactgctgc cggtatccaaa tcccaggcat aatgaatgat 360
 gaaaaattta acctgaagtt ggtcatcaaa ccagccaagg tcacccctgc accgactctg 420
 cagagagact tcactgcagc ctttccaagg atgcttacca ccagggggaca tggcccagca 480
 gagacacaga cactggggag cctccctgat ataatctaa cacaaatatt cacattggcc 540
 aatgagttac gggactctag attggccaat gacttacggg actctggagg aaccatcaga 600
 ataggcatct acatcggagc agggatctgt gctgggctgg ctctggetct tatcttcggc 660
 gctttaattt tcaaatggta ttctcatagc aaagagaaga tacagaattt aagcctcatc 720
 tctttggcca acctccctcc ctccaggattg gcaaatgcag tagcagaggg aattcgtcca 780
 gaagaaaaca tctataccat tgaagagaac gtatatgaag tggaggagcc caatgagtat 840
 tattgctatg tcagcagcag gcagcaaccc tcacaacctt tgggtgtgctg ctttgcaatg 900
 cca 903

<210> 38
 <211> 1704
 <212> DNA
 <213> Mus musculus

<220>
 <221> CAAT_signal
 <222> (1)..(1704)

<220>
 <221> CDS
 <222> (1)..(1701)

<400> 38
 atg att gac aga cag aga atg gga ctt tgg gct ttg gca att ctg aca 48
 Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
 1 5 10 15
 ctt ccc atg tat ttg aca gtt acg gag ggc agt aaa tcg tcc tgg ggt 96
 Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30
 ctg gaa aat gag gct tta att gtg aga tgc ccc caa aga gga cgc tcg 144
 Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
 35 40 45
 act tat cct gtg gaa tgg tat tac tca gat aca aat gaa agt att cct 192
 Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60
 act caa aaa aga aat cgg atc ttt gtc tca aga gat cgt ctg aag ttt 240
 Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80

cta cca gcc aga gtg gaa gac tct ggg att tat gct tgt gtt atc aga	288
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg	
85 90 95	
agc ccc aac ttg aat aag act gga tac ttg aat gtc acc ata cat aaa	336
Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys	
100 105 110	
aag ccg cca agc tgc aat atc cct gat tat ttg atg tac tcg aca gta	384
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val	
115 120 125	
cgt gga tca gat aaa aat ttc aag ata acg tgt cca aca att gac ctg	432
Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu	
130 135 140	
tat aat tgg aca gca cct gtt cag tgg ttt aag aac tgc aaa gct ctc	480
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu	
145 150 155 160	
caa gag cca agg ttc agg gca cac agg tcc tac ttg ttc att gac aac	528
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn	
165 170 175	
gtg act cat gat gat gaa ggt gac tac act tgt caa ttc aca cac gcg	576
Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala	
180 185 190	
gag aat gga acc aac tac atc gtg acg gcc acc aga tca ttc aca gtt	624
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val	
195 200 205	
gaa gaa aaa ggc ttt tct atg ttt cca gta att aca aat cct cca tac	672
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr	
210 215 220	
aac cac aca atg gaa gtg gaa ata gga aaa cca gca agt att gcc tgt	720
Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys	
225 230 235 240	
tca gct tgc ttt ggc aaa ggc tct cac ttc ttg gct gat gtc ctg tgg	768
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp	
245 250 255	
cag att aac aaa aca gta gtt gga aat ttt ggt gaa gca aga att caa	816
Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln	
260 265 270	
gaa gag gaa ggt cga aat gaa agt tcc agc aat gac atg gat tgt tta	864
Glu Glu Glu Gly Arg Asn Glu Ser Ser Asn Asp Met Asp Cys Leu	
275 280 285	
acc tca gtg tta agg ata act ggt gtg aca gaa aag gac ctg tcc ctg	912
Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu	
290 295 300	

gaa tat gac tgt ctg gcc ctg aac ctt cat ggc atg ata agg cac acc 960
 Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
 305 310 315 320
 ata agg ctg aga agg aaa caa cca att gat cac cga agc atc tac tac 1008
 Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr
 325 330 335
 ata gtt gct gga tgt agt tta ttg cta atg ttt atc aat gtc ttg gtg 1056
 Ile Val Ala Gly Cys Ser Leu Leu Leu Met Phe Ile Asn Val Leu Val
 340 345 350
 ata gtc tta aaa gtg ttc tgg att gag gtt gct ctg ttc tgg aga gat 1104
 Ile Val Leu Lys Val Phe Trp Ile Glu Val Ala Leu Phe Trp Arg Asp
 355 360 365
 ata gtg aca cct tac aaa acc cgg aac gat ggc aag ctc tac gat gcg 1152
 Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala
 370 375 380
 tac atc att tac cct cgg gtc ttc cgg ggc agc gcg gcg gga acc cac 1200
 Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly Thr His
 385 390 395 400
 tct gtg gag tac ttt gtt cac cac act ctg ccc gac gtt ctt gaa aat 1248
 Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu Glu Asn
 405 410 415
 aaa tgt ggc tac aaa ttg tgc att tat ggg aga gac ctg tta cct ggg 1296
 Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu Pro Gly
 420 425 430
 caa gat gca gcc acc gtg gtg gaa agc agt atc cag aat agc aga aga 1344
 Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser Arg Arg
 435 440 445
 cag gtg ttt gtt ctg gcc cct cac atg atg cac agc aag gaa ttt gcc 1392
 Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala
 450 455 460
 tac gag cag gag att gct ctg cac agc gcc ctc atc cag aac aac tcc 1440
 Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser
 465 470 475 480
 aag gtg att ctt att gaa atg gag cct ctg ggt gag gca agc cga cta 1488
 Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser Arg Leu
 485 490 495
 cag gtt ggg gac ctg caa gat tct ctc cag cat ctt gtg aaa att cag 1536
 Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Ile Gln
 500 505 510
 ggg acc atc aag tgg agg gaa gat cat gtg gcc gac aag cag tct cta 1584
 Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu
 515 520 525

agt tcc aaa ttc tgg aag cat gtg agg tac caa atg cca gtg cca gaa 1632
 Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
 530 535 540

aga gcc tcc aag acg gca tct gtt gcg gct ccg ttg agt ggc aag gca 1680
 Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Ala
 545 550 555 560

tgc tta gac ctg aaa cac ttt tga 1704
 Cys Leu Asp Leu Lys His Phe
 565

<210> 39
 <211> 567
 <212> PRT
 <213> Mus musculus

<400> 39
 Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
 1 5 10 15

Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30

Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
 35 40 45

Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60

Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80

Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
 85 90 95

Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
 100 105 110

Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
 115 120 125

Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
 130 135 140

Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
 145 150 155 160

Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
 165 170 175

Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
 180 185 190

Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
 195 200 205

Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
 210 215 220
 Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
 225 230 235 240
 Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
 245 250 255
 Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
 260 265 270
 Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
 275 280 285
 Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
 290 295 300
 Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
 305 310 315 320
 Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr
 325 330 335
 Ile Val Ala Gly Cys Ser Leu Leu Leu Met Phe Ile Asn Val Leu Val
 340 345 350
 Ile Val Leu Lys Val Phe Trp Ile Glu Val Ala Leu Phe Trp Arg Asp
 355 360 365
 Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala
 370 375 380
 Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly Thr His
 385 390 395 400
 Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu Glu Asn
 405 410 415
 Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu Pro Gly
 420 425 430
 Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser Arg Arg
 435 440 445
 Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala
 450 455 460
 Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser
 465 470 475 480
 Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser Arg Leu
 485 490 495
 Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Ile Gln
 500 505 510

Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu
 515 520 525

Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
 530 535 540

Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Ala
 545 550 555 560

Cys Leu Asp Leu Lys His Phe
 565

<210> 40
 <211> 1029
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1026)

<400> 40
 atg att gac aga cag aga atg gga ctt tgg gct ttg gca att ctg aca 48
 Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
 1 5 10 15

ctt ccc atg tat ttg aca gtt acg gag ggc agt aaa tcg tcc tgg ggt 96
 Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30

ctg gaa aat gag gct tta att gtg aga tgc ccc caa aga gga cgc tcg 144
 Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
 35 40 45

act tat cct gtg gaa tgg tat tac tca gat aca aat gaa agt att cct 192
 Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60

act caa aaa aga aat cgg atc ttt gtc tca aga gat cgt ctg aag ttt 240
 Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80

cta cca gcc aga gtg gaa gac tct ggg att tat gct tgt gtt atc aga 288
 Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
 85 90 95

agc ccc aac ttg aat aag act gga tac ttg aat gtc acc ata cat aaa 336
 Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
 100 105 110

aag cgg cca agc tgc aat atc cct gat tat ttg atg tac tcg aca gta 384
 Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
 115 120 125

cgt gga tca gat aaa aat ttc aag ata acg tgt cca aca att gac ctg 432
 Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
 130 135 140

tat aat tgg aca gca cct gtt cag tgg ttt aag aac tgc aaa gct ctc	480
Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu	
145 150 155 160	
caa gag cca agg ttc agg gca cac agg tcc tac ttg ttc att gac aac	528
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn	
165 170 175	
gtg act cat gat gat gaa ggt gac tac act tgt caa ttc aca cac gcg	576
Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala	
180 185 190	
gag aat gga acc aac tac atc gtg acg gcc acc aga tca ttc aca gtt	624
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val	
195 200 205	
gaa gaa aaa ggc ttt tct atg ttt cca gta att aca aat cct cca tac	672
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr	
210 215 220	
aac cac aca atg gaa gtg gaa ata gga aaa cca gca agt att gcc tgt	720
Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys	
225 230 235 240	
tca gct tgc ttt ggc aaa ggc tct cac ttc ttg gct gat gtc ctg tgg	768
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp	
245 250 255	
cag att aac aaa aca gta gtt gga aat ttt ggt gaa gca aga att caa	816
Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln	
260 265 270	
gaa gag gaa ggt cga aat gaa agt tcc agc aat gac atg gat tgt tta	864
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu	
275 280 285	
acc tca gtg tta agg ata act ggt gtg aca gaa aag gac ctg tcc ctg	912
Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu	
290 295 300	
gaa tat gac tgt ctg gcc ctg aac ctt cat ggc atg ata agg cac acc	960
Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr	
305 310 315 320	
ata agg ctg aga agg aaa caa cca att gat cac cga agc atc tac tac	1008
Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr	
325 330 335	
ata gtt gct gga tgt agt tga	1029
Ile Val Ala Gly Cys Ser	
340	

<210> 41
 <211> 342
 <212> PRT
 <213> Mus musculus

<400> 41

Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
 1 5 10 15

Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
 20 25 30

Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
 35 40 45

Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
 50 55 60

Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
 65 70 75 80

Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
 85 90 95

Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
 100 105 110

Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
 115 120 125

Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
 130 135 140

Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
 145 150 155 160

Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
 165 170 175

Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
 180 185 190

Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
 195 200 205

Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
 210 215 220

Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
 225 230 235 240

Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
 245 250 255

Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
 260 265 270

Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
 275 280 285

Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
 290 295 300

Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
305 310 315 320

Ile Arg Leu Arg Arg Lys Gln Pro Ile Asp His Arg Ser Ile Tyr Tyr
325 330 335

Ile Val Ala Gly Cys Ser
340

<210> 42
<211> 606
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(603)

<400> 42
aga gat ata gtg aca cct tac aaa acc cgg aac gat ggc aag ctc tac 48
Arg Asp Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr
1 5 10 15
gat gcg tac atc att tac cct cgg gtc ttc cgg ggc agc gcg gcg gga 96
Asp Ala Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly
20 25 30
acc cac tct gtg gag tac ttt gtt cac cac act ctg ccc gac gtt ctt 144
Thr His Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu
35 40 45
gaa aat aaa tgt ggc tac aaa ttg tgc att tat ggg aga gac ctg tta 192
Glu Asn Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu
50 55 60
cct ggg caa gat gca gcc acc gtg gtg gaa agc agt atc cag aat agc 240
Pro Gly Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser
65 70 75 80
aga aga cag gtg ttt gtt ctg gcc cct cac atg atg cac agc aag gaa 288
Arg Arg Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu
85 90 95
ttt gcc tac gag cag gag att gct ctg cac agc gcc ctc atc cag aac 336
Phe Ala Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn
100 105 110
aac tcc aag gtg att ctt att gaa atg gag cct ctg ggt gag gca agc 384
Asn Ser Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser
115 120 125
cga cta cag gtt ggg gac ctg caa gat tct ctc cag cat ctt gtg aaa 432
Arg Leu Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys
130 135 140

att cag ggg acc atc aag tgg agg gaa gat cat gtg gcc gac aag cag 480
 ile Gln Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln
 145 150 155 160

tct cta agt tcc aaa ttc tgg aag cat gtg agg tac caa atg cca gtg 528
 Ser Leu Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val
 165 170 175

cca gaa aga gcc tcc aag acg gca tct gtt gcg gct ccg ttg agt ggc 576
 Pro Glu Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly
 180 185 190

aag gca tgc tta gac ctg aaa cac ttt tga 606
 Lys Ala Cys Leu Asp Leu Lys His Phe
 195 200

<210> 43
 <211> 201
 <212> PRT
 <213> Mus musculus

<400> 43
 Arg Asp Ile Val Thr Pro Tyr Lys Thr Arg Asn Asp Gly Lys Leu Tyr
 1 5 10 15

Asp Ala Tyr Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly
 20 25 30

Thr His Ser Val Glu Tyr Phe Val His His Thr Leu Pro Asp Val Leu
 35 40 45

Glu Asn Lys Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu
 50 55 60

Pro Gly Gln Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser
 65 70 75 80

Arg Arg Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu
 85 90 95

Phe Ala Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn
 100 105 110

Asn Ser Lys Val Ile Leu Ile Glu Met Glu Pro Leu Gly Glu Ala Ser
 115 120 125

Arg Leu Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys
 130 135 140

Ile Gln Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln
 145 150 155 160

Ser Leu Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val
 165 170 175

Pro Glu Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly
 180 185 190

Lys Ala Cys Leu Asp Leu Lys His Phe
195 200

<210> 44
<211> 1357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (47)..(1030)

<400> 44
atctcaacaa cgagttacca atacttgctc ttgattgata aacaga atg ggg ttt 55
Met Gly Phe
1

tgg atc tta gca att ctc aca att ctc atg tat tcc aca gca gca aag 103
Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr Ala Ala Lys
5 10 15

ttt agt aaa caa tca tgg ggc ctg gaa aat gag gct tta att gta aga 151
Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu Ile Val Arg
20 25 30 35

tgt cct aga caa gga aaa cct agt tac acc gtg gat tgg tat tac tca 199
Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp Tyr Tyr Ser
40 45 50

caa aca aac aaa agt att ccc act cag gaa aga aat cgt gtg ttt gcc 247
Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg Val Phe Ala
55 60 65

tca ggc caa ctt ctg aag ttt cta cca gct gaa gtt gct gat tct ggt 295
Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala Asp Ser Gly
70 75 80

att tat acc tgt att gtc aga agt ccc aca ttc aat agg act gga tat 343
Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg Thr Gly Tyr
85 90 95

gcg aat gtc acc ata tat aaa aaa caa tca gat tgc aat gtt cca gat 391
Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn Val Pro Asp
100 105 110 115

tat ttg atg tat tca aca gta tct gga tca gaa aaa aat tcc aaa att 439
Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn Ser Lys Ile
120 125 130

tat tgt cct acc att gac ctc tac aac tgg aca gca cct ctt gag tgg 487
Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro Leu Glu Trp
135 140 145

ttt aag aat tgt cag gct ctt caa gga tca agg tac agg gcg cac aag 535
Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg Ala His Lys
150 155 160

tca ttt ttg gtc att gat aat gtg atg act gag gac gca ggt gat tac 583
Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala Gly Asp Tyr
165 170 175

acc tgt aaa ttt ata cac aat gaa aat gga gcc aat tat agt gtg acg 631
Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr Ser Val Thr
180 185 190 195

gcg acc agg tcc ttc acg gtc aag gat gag caa ggc ttt tct ctg ttt 679
Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe Ser Leu Phe
200 205 210

cca gta atc gga gcc cct gca caa aat gaa ata aag gaa gtg gaa att 727
Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu Val Glu Ile
215 220 225

gga aaa aac gca aac cta act tgc tct gct tgt ttt gga aaa ggc act 775
Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly Lys Gly Thr
230 235 240

cag ttc ttg gct gcc gtc ctg tgg cag ctt aat gga aca aaa att aca 823
Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr Lys Ile Thr
245 250 255

gac ttt ggt gaa cca aga att caa caa gag gaa ggg caa aat caa agt 871
Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln Asn Gln Ser
260 265 270 275

ttc agc aat ggg ctg gct tgt cta gac atg gtt tta aga ata gct gac 919
Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg Ile Ala Asp
280 285 290

gtg aag gaa gag gat tta ttg ctg cag tac gac tgt ctg gcc ctg aat 967
Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu Ala Leu Asn
295 300 305

ttg cat ggc ttg aga agg cac acc gta aga cta agt agg aaa aat cca 1015
Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg Lys Asn Pro
310 315 320

agt aag gag tgt ttc tgagactttg atcacctgaa ctttctctag caagtgtgaa 1070
Ser Lys Glu Cys Phe
325

cagaatggag tgtggttcca agagatccat caagacaatg ggaatggcct gtgccataaa 1130
atgtgcttct cttctctogg atgttggttg ctgtctgac tttgtagact gtctctgttt 1190
gctgggagct tctctgctgc ttaaattggt cgtctctccc cactccctcc tatcgttggt 1250
ttgtctagaa cactcagctg cttctttggt catcctgttt ttctaacttt atgaactccc 1310
tctgtgtcac tgtatgtgaa aggaaatgca ccaacaacgg aaaactg 1357

<210> 45
<211> 328
<212> PRT

<213> Homo sapiens

<400> 45

Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
1 5 10 15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
20 25 30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
35 40 45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
50 55 60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65 70 75 80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
85 90 95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
100 105 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
115 120 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
130 135 140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145 150 155 160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
165 170 175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
180 185 190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
195 200 205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
210 215 220
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225 230 235 240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
245 250 255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
260 265 270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
275 280 285

Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
290 295 300

Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305 310 315 320

Lys Asn Pro Ser Lys Glu Cys Phe
325

<210> 46
<211> 72
<212> DNA
<213> Mus musculus

<400> 46
ttattgctaa tgttatcaa tgtcttggtg atagtcttaa aagtgttctg gattgaggtt 60
gctctgttct gg 72

<210> 47
<211> 1011
<212> DNA
<213> Mus musculus

<400> 47
atgattgaca gacagagaat gggactttgg gctttggcaa ttctgacact tcccatgtat 60
ttgacagtta cggaggggcag taaatcgtec tgggtctctg aaaatgaggc ttaattgtg 120
agatgcccc aaagaggacg ctgcacttat cctgtggaat ggtattactc agatacaaat 180
gaaagtattc ctactcaaaa aagaaatcgg atctttgtct caagagatcg tctgaagttt 240
ctaccagcca gagtcaaga ctctgggatt tatgcttggt ttatcagaag cccaacttg 300
aataagactg gatacttgaa tgtcaccata cataaaaagc cgccaagctg caatatccct 360
gattatttga tgtactcgac agtacgtgga tcagataaaa atttcaagat aagctgtcca 420
acaattgacc tgtataattg gacagcacct gtctcagtggt ttaagaactg caaagctctc 480
caagagccaa ggttcagggc acacagggtc tacttggtca ttgacaacgt gactcatgat 540
gatgaaggtg actacacttg tcaattcaca caccgggaga atggaaccaa ctacatcggt 600
acggccacca gatcattcac agttgaagaa aaaggctttt ctatgtttcc agtaattaca 660
aatcctccat acaaccacac aatggaagtg gaaataggaa aaccagcaag tattgcctgt 720
tcagcttgct ttggcaaaag ctctcacttc ttggctgatg tcctgtggca gattaacaaa 780
acagttagtg gaaatttttg tgaagcaaga attcaagaag aggaaggtcg aaatgaagt 840
tccagcaatg acatggattg ttaacctca gtgttaagga taactggtgt gacagaaaag 900
gacctgtccc tggaatatga ctgtctggcc ctgaaccttc atggcatgat aaggcacacc 960

ataaggctga gaaggaaaca accaagtaag gagtgctcct cacacattgc t

1011

<210> 48

<211> 337

<212> PRT

<213> Mus musculus

<400> 48

Met	Ile	Asp	Arg	Gln	Arg	Met	Gly	Leu	Trp	Ala	Leu	Ala	Ile	Leu	Thr
1				5					10					15	
Leu	Pro	Met	Tyr	Leu	Thr	Val	Thr	Glu	Gly	Ser	Lys	Ser	Ser	Trp	Gly
			20					25						30	
Leu	Glu	Asn	Glu	Ala	Leu	Ile	Val	Arg	Cys	Pro	Gln	Arg	Gly	Arg	Ser
		35					40					45			
Thr	Tyr	Pro	Val	Glu	Trp	Tyr	Tyr	Ser	Asp	Thr	Asn	Glu	Ser	Ile	Pro
	50					55					60				
Thr	Gln	Lys	Arg	Asn	Arg	Ile	Phe	Val	Ser	Arg	Asp	Arg	Leu	Lys	Phe
	65				70					75					80
Leu	Pro	Ala	Arg	Val	Glu	Asp	Ser	Gly	Ile	Tyr	Ala	Cys	Val	Ile	Arg
				85					90					95	
Ser	Pro	Asn	Leu	Asn	Lys	Thr	Gly	Tyr	Leu	Asn	Val	Thr	Ile	His	Lys
		100						105					110		
Lys	Pro	Pro	Ser	Cys	Asn	Ile	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val
		115					120						125		
Arg	Gly	Ser	Asp	Lys	Asn	Phe	Lys	Ile	Thr	Cys	Pro	Thr	Ile	Asp	Leu
	130					135						140			
Tyr	Asn	Trp	Thr	Ala	Pro	Val	Gln	Trp	Phe	Lys	Asn	Cys	Lys	Ala	Leu
	145				150					155					160
Gln	Glu	Pro	Arg	Phe	Arg	Ala	His	Arg	Ser	Tyr	Leu	Phe	Ile	Asp	Asn
			165						170					175	
Val	Thr	His	Asp	Asp	Glu	Gly	Asp	Tyr	Thr	Cys	Gln	Phe	Thr	His	Ala
			180					185					190		
Glu	Asn	Gly	Thr	Asn	Tyr	Ile	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val
		195					200					205			
Glu	Glu	Lys	Gly	Phe	Ser	Met	Phe	Pro	Val	Ile	Thr	Asn	Pro	Pro	Tyr
	210					215					220				
Asn	His	Thr	Met	Glu	Val	Glu	Ile	Gly	Lys	Pro	Ala	Ser	Ile	Ala	Cys
	225				230					235					240
Ser	Ala	Cys	Phe	Gly	Lys	Gly	Ser	His	Phe	Leu	Ala	Asp	Val	Leu	Trp
			245						250				255		

Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
260 265 270

Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
275 280 285

Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
290 295 300

Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
305 310 315 320

Ile Arg Leu Arg Arg Lys Gln Pro Ser Lys Glu Cys Pro Ser His Ile
325 330 335

Ala

<210> 49
<211> 337
<212> PRT
<213> Mus musculus

<400> 49
Met Ile Asp Arg Gln Arg Met Gly Leu Trp Ala Leu Ala Ile Leu Thr
1 5 10 15

Leu Pro Met Tyr Leu Thr Val Thr Glu Gly Ser Lys Ser Ser Trp Gly
20 25 30

Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Arg Ser
35 40 45

Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
50 55 60

Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65 70 75 80

Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
85 90 95

Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
100 105 110

Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
115 120 125

Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
130 135 140

Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
145 150 155 160

Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
165 170 175

Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
 180 185 190
 Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
 195 200 205
 Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
 210 215 220
 Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
 225 230 235 240
 Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
 245 250 255
 Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
 260 265 270
 Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
 275 280 285
 Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
 290 295 300
 Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
 305 310 315 320
 Ile Arg Leu Arg Arg Lys Gln Pro Ser Lys Glu Cys Pro Ser His Ile
 325 330 335

Ala